

FIG. 1

ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG TTT ACG GTC AGT TTG GCA Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala 1 5 10 15	48
TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT CAA AGA GAG AAA CAT AAC Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn 20 25 30	96
GGC GGT AGA GGG GAA GTC ACC AAG GTT GCC ACT CAG AAG CAC CGA CAG Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln 35 40 45	144
TCA CCG CTT AAC TGG ACC TCC AGT CAT TTC GGA GAG GTG ACT GGG AGC Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser 50 55 60	192
GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC CCC TAC TCC CGG GCT TTC Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe 65 70 75 80	240
GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC TGC AGG AAC GGC GGT ACC Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr 85 90 95	288
TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG GCC CAC TTC ACC GGC CGC Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg 100 105 110	336
TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA TGC GGC GCC CTG GAG CAC Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His 115 120 125	384
GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC TGC AGG TGC ATC TTC GGG Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly 130 135 140	432
GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT GAC CGC TGT GAC CCG AAA Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys 145 150 155 160	480
GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG AGC GCC GGG GGC GCG CCC Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro 165 170 175	528
AGC CTG CTA CTC TTG CTG CCC TGC GCA CTC CTG CAC CGC CTC CTG CGC Ser Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg 180 185 190	576
CCG GAT GCG CCC GCG CAC CCT CGG TCC CTG GTC CCT TCC GTC CTC CAG Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln 195 200 205	624
CGG GAG CGG CGC CCC TGC GGA AGG CCG GGA CTT GGG CAT CGC CTT TAA Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu * 210 215 220	672

FIG. 2

AMINO ACID ALIGNMENT BETWEEN CRIPTO AND CRIPTIN

		10		20		30		40																																	
1	M	T	W	R	H	H	V	R	L	L	F	T	V	S	L	A	L	Q	I	I	N	L	G	N	S	Y	Q	R	E	K	H	N	G	G	R	G	E	V	T	K	HGS Cryptin
1	M	-	-	H	A	A	I	S	K	V	F	E	L	G	L	-	-	-	V	A	G	L	G	-	-	-	H	Q	E	F	A	R	P	S	R	G	Y	L	A	-	Human Crip
		50		60		70		80																																	
41	V	A	T	Q	K	H	R	Q	S	P	L	N	W	T	S	S	H	F	G	E	V	T	G	S	A	E	G	W	G	P	E	E	P	L	P	Y	S	R	A	F	HGS Cryptin
32	-	-	-	-	-	F	R	D	D	S	I	-	W	P	Q	E	E	-	P	A	I	R	P	R	S	S	Q	R	V	P	P	M	G	I	Q	H	S	K	E	L	Human Crip
		90		100		110		120																																	
81	G	E	G	A	S	A	R	P	R	C	C	R	N	G	G	T	C	V	L	G	S	F	C	V	C	P	A	H	F	T	G	R	Y	C	E	H	D	Q	R	R	HGS Cryptin
65	N	R	T	-	-	-	-	-	-	C	C	L	N	G	G	T	C	M	L	G	S	F	C	A	C	P	P	S	F	Y	G	R	N	C	E	H	D	V	R	K	Human Crip
		130		140		150		160																																	
121	S	E	C	G	A	L	E	H	G	A	W	T	L	R	A	C	H	L	C	R	C	I	F	G	A	L	H	C	L	P	L	Q	T	P	D	R	C	D	P	-	HGS Cryptin
99	E	N	C	G	S	V	P	H	D	T	W	L	P	K	K	C	S	L	C	K	C	W	H	G	Q	L	R	C	F	P	Q	A	F	L	P	G	C	D	G	L	Human Crip
		170		180		190		200																																	
160	-	-	-	K	D	F	L	A	S	H	A	H	G	-	P	S	A	G	G	A	P	S	L	L	L	L	P	C	A	L	L	H	R	L	L	R	P	D	A	HGS Cryptin	
139	V	M	D	E	H	L	V	A	S	R	T	P	E	L	P	P	S	A	R	T	T	T	F	L	M	V	G	I	C	L	S	I	Q	S	Y					Human Crip	
		210		220																																					
196	P	A	H	P	R	S	L	V	P	S	V	L	Q	R	E	R	R	P	C	G	R	P	G	L	G	H	R	L												HGS Cryptin	
174																																									Human Crip

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.